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Fingerprint pattern similarity: a family-based study using novel classification

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Abstract

Objectives: Establishing that certain traits are inherited can be assessed from the extent of morphological similarity of the offspring and their parents. This study, evaluated the pattern similarity of the fingerprint of offspring to that of their parents using a novel classification.

Methods: Fifty families (comprising of father, mother and a child) without ethnic considerations were recruited and digital fingerprints were obtained. The fingerprints; arch (A), loop (L), and whorl (W) were identified and a novel classification (A, L, W, AL, AW, and LW) for heredity study as described by Aigbogun et al.(2018) was adopted. Chi-square analysis was used to test distribution differences, while a pedigree tree was designed for the offspring's similarity to the parents.

Results: In this study, loop (L) was consistently predominant both as single (>60%) and combined distribution (>75%), followed by whorl (<25%) and then arch (<22%); although not entirely consistent for the whorl (W) and arch (A). The distribution except the ring finger (χ^2=24.891; P=0.036) was not statistically significant (p>0.05). From the pedigree tree, the possibility that the offspring displayed patterns similar to that of the parental combinations was 84% for the thumb, 76% for the index finger, 84% for the middle finger, 88% for the ring finger, and 92% for the little finger.

Conclusion: Morphological evidence from this study suggests that fingerprints are more genetically determined than environmentally influenced; however, the pattern in which they are inherited seemed closer to co-recessivity with complex expressivity.

Keywords: family; fingerprint pattern; human; inheritance; novel classification

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Introduction

The argument about the heritability of certain traits including fingerprints in humans has been on for years. Geneticists have established that nearly all traits in the offspring are shared genetic information from the parents;[1] however, the nature in which these traits are expressed are to a great extent dependent on how they are inherited and the susceptibility to exogenous interference, such as diseases, mutation, and environment.[2,3] Establishing the fact that certain traits are inherited in a particular fashion provide the basis for predicting the outcome of an offspring and vice versa. The hereditary implication of fingerprints has drawn attention from geneticists for a long while, because it is believed that they hold valuable information capable of explaining various familial characteristics and diseases.[4–10]

The ridge-like impressions noticeable on all the fingers are called fingerprint (friction ridges) and its study is called dermatoglyphics.[11,12] Although the number, shape, indentations, and spacing of the ridges varies from one individual to another,[13–16] it is suggested that the ridge patterns are partly genetically determined and environmentally influenced;[17–19] hence, fingerprint is believed to be a multifactorial trait.[20]

Scientific evidence regarding the fingerprint pattern similarity in families using the qualitative attributes is relatively scarce, because most studies utilized the quantitative methods,[19,21–23] and the available classifications did not provide enough scientific basis for its use in family-based studies. This study, therefore, evaluated the fingerprint pattern similarity between the parents and offspring using a novel classification technique.

Materials and Methods

The study adopted a cross-sectional design, which involved the collection of the digital fingerprint from 50 randomly-selected families in Rivers State, Nigeria to estimate the pattern similarity of the offspring to that of the parents using novel classification.

Stratified random sampling was adopted for the study. This considered the concentration of residential areas with mainly civil servants and employees of higher institutions, which made it easier to get a complete sample population (family size), explain the study, and get consent. Volunteer families were conveniently sampled from across various residential areas in Port Harcourt, Rivers State, Nigeria. The study did not take into consideration the ethnicity of the families; however, the study utilized only families of Nigerian descent. The criteria for selection included families with at least father, mother and a child, and no clinical or medical history of congenital abnormalities. Incomplete families (single parents or no child), family with a history of adoption, and damaged anatomical parts of choice were all excluded from the study. In a situation where a family had more than a child, to reduce sample bias, simple paper balloting was used to determine which offspring participated in the study. The age of the participating families was a selection criterion only for infant children (less than 2 years), but when fingerprint obscurity was noticed in the parent, the family was excluded; however, when it affected an offspring and the family had more than one, the next offspring was chosen as a replacement.

Digital fingerprints were obtained using the HP Scanjet 300 Flatbed Photo Scanner as described by Aigbogun et al.[24] The palm of the hands was wiped thoroughly, before placing on the screen of the scanner. A little pressure was applied when the palm was placed on the surface of the scanner, for adequate contact with the fingers. Only the primary fingerprint details were required; therefore, the palm and all five digits were taken together in one scan as illustrated in **Figure 1**. After each print, sterile tissue wipes were used to clean the glass-scanning surface to prevent contamination. The digit prints were read directly from the picture (**Figure 1**) and the print patterns entered into an excel sheet, which was tabulated and stratified by families. The study utilized the three general classification types; arch (A), loop (L) and whorl (W) for all digits of the right (R) and left (L) hand.[25]

This study adopted Aigbogun et al. classification to organize the fingerprint patterns and distributions.[26] In this technique, when considering hereditary of fingerprint pattern, it is assumed that both right and left digits are a unit. For easy identification, the study considered the alphabetic positions as follows: A (both hands arch), L (both hands loop), W (both hands whorl), AL (arch-loop combinations on either hand), AW (arch-whorl combinations on either hand), and LW (loop-whorl combination on either hand).[26]

Using the Excel Sheet, each trait (pattern combination) of the parents (as a single group) were tabulated against the possible combination outcome (by crosses) of their offspring and a pedigree tree drawn for all parental

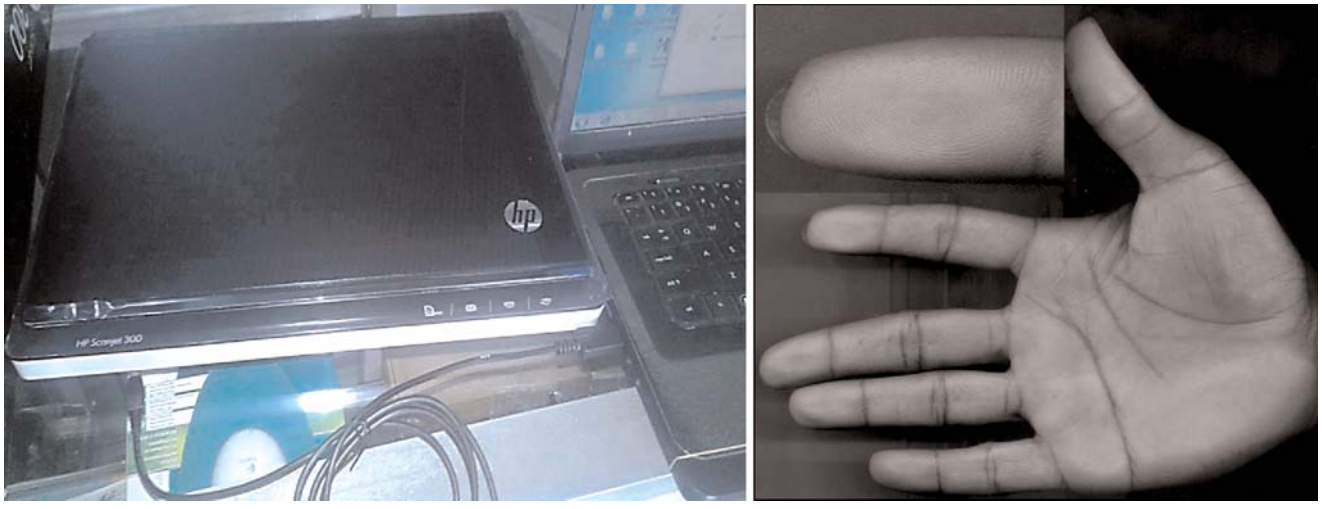

Figure 1. Digital hand print obtained using the HP 300 flatbed scanner (zoomed in to capture fingerprint type).[24] [Color figure can be viewed in the online issue, which is available at www.anatomy.org.tr]

Table 1
The distribution of dermatoglyphic pattern on the thumb and test of association.

		Thumb (1D)			Chi-square analysis			
Side	**Group**	**A**	**L**	**W**	**Df**	**χ^2**	**p**	**Inference**
Right	Father	4 (8.0)	38 (76.0)	8 (16.0)				
	Mother	9 (18.0)	35 (70.0)	6 (12.0)	4	3.34	0.503	NS
	Offspring	10 (20.0)	33 (66.0)	7 (14.0)				
	Total	**23 (15.3)**	**106 (70.7)**	**21 (14.0)**				
Left	Father	8 (16.0)	36 (72.0)	6 (12.0)				
	Mother	14 (28.0)	30 (60.0)	6 (12.0)	4	5.594	0.232	NS
	Offspring	16 (32.0)	25 (50.0)	9 (18.0)				
	Total	**38 (25.3)**	**91 (60.7)**	**21 (14.0)**				

A: arch; **Df:** degree of freedom; **L:** loop; **NS:** non-significant; **W:** whorl; **χ^2**: chi-square value.

combinations and offspring outcome. Statistical Package for Social Sciences (SPSS for Windows, version 23.0, Armonk, New York, USA) was used for chi-square analysis to present distribution and analyse association (confidence level set at 95%, and $p<0.05$ was considered significant). The percentage conformance of offspring to parental combinations was calculated.

The study obtained ethical clearance (with reference number UPH/R&D/REC/026) from the University Ethics Committee of the Post-Graduate School of the University of Por Harcourt; after review by the Departmental Post-Graduate Board. Participating families (the parents, on behalf of the families) provided a written and signed informed consent after a clear explanation of the research purpose, procedure and benefits. The study adhered to all statutory and regulatory requirements for human participation in research(es).

Results

The distribution of the fingerprint patterns (stratified by the family components), and the Chi-square test of distributional differences of the patterns on both hands (right and left) are shown in **Tables 1–5**. The parental combinations of the fingerprint patterns and outcome in offspring (conformity; as straight black lines and nonconformity; as dotted red lines), as well as percentage predictability of the outcome for each finger are shown in **Figures 1–5**.

The loop pattern dominated in all fingers; thumb (1D) [R; 70.7%, L; 60.7%], index (2D) [R; 55.3%, L; 59.3%], middle (3D) [R; 68.7%, L; 70.7%], ring (4D) [R; 66.0%, L; 69.3%], little (5D) [R; 66.0%, L; 69.3%]. The distribution of the fingerprints on the right and left fingers were not statistically significant ($p>0.05$) in the family strata, except for the right ring finger ($\chi^2=10.549$; $p=0.032$) (**Tables 1–5**).

Table 2
The distribution of dermatoglyphic pattern on the index finger and test of association.

		Index (2D)			Chi-square analysis			
Side	**Group**	**A**	**L**	**W**	**Df**	**χ^2**	**p**	**Inference**
Right	Father	11 (22.0)	27 (54.0)	12 (24.0)				
	Mother	7 (14.0)	32 (64.0)	11 (22.0)	4	3.550	0.470	NS
	Offspring	14 (28.0)	24 (48.0)	12 (24.0)				
	Total	**32 (21.3)**	**83 (55.3)**	**35 (23.3)**				
Left	Father	8 (16.0)	32 (64.0)	10 (20.0)				
	Mother	13 (26.0)	29 (58.0)	8 (16.0)	4	2.371	0.668	NS
	Offspring	14 (28.0)	28 (56.0)	8 (16.0)				
	Total	**35 (23.3)**	**89 (59.3)**	**26 (17.3)**				

A: arch; **Df:** degree of freedom; **L:** loop; **NS:** non-significant; **W:** whorl; **χ^2**: chi-square value.

Table 3
The distribution of dermatoglyphic pattern on the middle finger and test of association.

		Middle (3D)			Chi-square analysis			
Side	**Group**	**A**	**L**	**W**	**Df**	**χ^2**	**p**	**Inference**
Right	Father	5 (10.0)	33 (66.0)	12 (24.0)				
	Mother	6 (12.0)	37 (74.0)	7 (14.0)	4	3.166	0.530	NS
	Offspring	9 (18.0)	33 (66.0)	8 (16.0)				
	Total	**20 (13.3)**	**103 (68.7)**	**27 (18.0)**				
Left	Father	6 (12.0)	33 (66.0)	11 (22.0)				
	Mother	4 (8.0)	39 (78.0)	7 (14.0)	4	6.734	0.151	NS
	Offspring	11 (22.0)	34 (68.0)	5 (10.0)				
	Total	**21 (14.0)**	**106 (70.7)**	**23 (15.3)**				

A: arch; **Df:** degree of freedom; **L:** loop; **NS:** non-significant; **W:** whorl; χ^2: chi-square value.

Table 4
The distribution of dermatoglyphic pattern on the ring finger and test of association.

		Ring (4D)			Chi-square analysis			
Side	**Group**	**A**	**L**	**W**	**Df**	**χ^2**	**p**	**Inference**
Right	Father	4 (8.0)	26 (52.0)	20 (40.0)				
	Mother	5 (10.0)	39 (78.0)	6 (12.0)	4	10.549	**0.032**	S
	Offspring	4 (8.0)	34 (68.0)	12 (24.0)				
	Total	**13 (8.7)**	**99 (66.0)**	**38 (25.3)**				
Left	Father	1 (2.0)	33 (66.0)	16 (32.0)				
	Mother	4 (8.0)	39 (78.0)	7 (14.0)	4	7.767	0.100	NS
	Offspring	6 (12.0)	32 (64.0)	12 (24.0)				
	Total	**11 (7.3)**	**104 (69.3)**	**35 (23.3)**				

A: arch; **Df:** degree of freedom; **L:** loop; **NS:** non-significant; **S:** significant; **W:** whorl; χ^2: chi-square value.

Table 5
TThe distribution of dermatoglyphic pattern on the little finger and test of association.

		Little (5D)			Chi-square analysis			
Side	**Group**	**A**	**L**	**W**	**Df**	**χ^2**	**p**	**Inference**
Right	Father	3 (6.0)	41 (82.0)	6 (12.0)				
	Mother	2 (4.0)	46 (92.0)	2 (4.0)	4	2.576	0.631	NS
	Offspring	3 (6.0)	42 (84.0)	5 (10.0)				
	Total	**8 (5.3)**	**129 (86.0)**	**13 (8.7)**				
Left	Father	3 (6.0)	43 (86.0)	4 (8.0)				
	Mother	5 (10.0)	42 (84.0)	3 (6.0)	4	1.902	0.754	NS
	Offspring	5 (10.0)	39 (78.0)	6 (12.0)				
	Total	**13 (8.7)**	**124 (82.7)**	**13 (8.7)**				

A: arch; **Df:** degree of freedom; **L:** loop; **NS:** non-significant; **W:** whorl; χ^2: chi-square value.

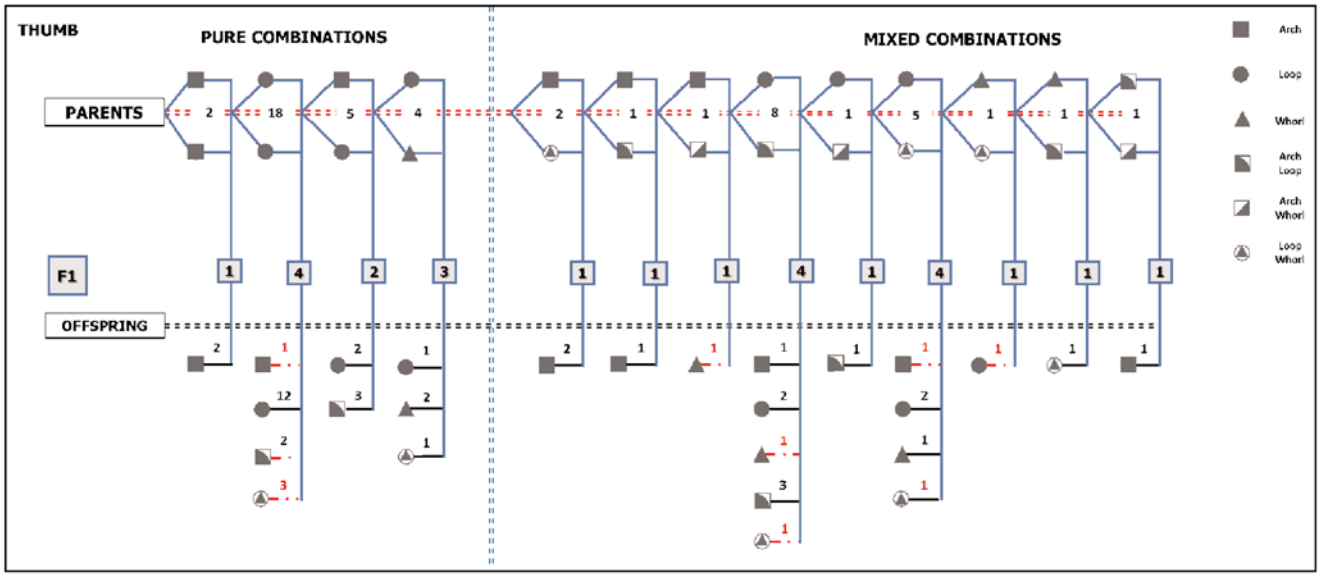

Figure 2. Pedigree tree and offspring patterns from parental combinations on the thumb (offspring conformity to parental combination; black color: yes, red color: no; [39/50=78% possibility of inheritance]). [Color figure can be viewed in the online issue, which is available at www.anatomy.org.tr]

From the cross-match, the study showed that only the index and ring fingers presented all possible combinations for the patterns (A, L, W, AL, AW, and LW), while on other fingers (thumb, middle and ring), the pattern AW was absent (**Figures 2–6**). The parental combination on the thumb (1D) displayed 13 patterns, with the offspring presenting a 78% conformance (39 matching outcomes of the 50 offspring fingerprint and 11 outcomes not matching parental combinations; **Figure 2**). The parental combination on the index finger displayed 14 patterns, with 76% conformance (38 matching and 11 outliners; **Figure 3**), while the parental combination on the middle finger had 11 patterns and 84% conformance (42 matching and 8 outliners; **Figure 4**). The parental combination on the ring finger displayed 9 patterns with 88% conformance (44 matching and 6 outliners; **Figure 5**), whereas, the

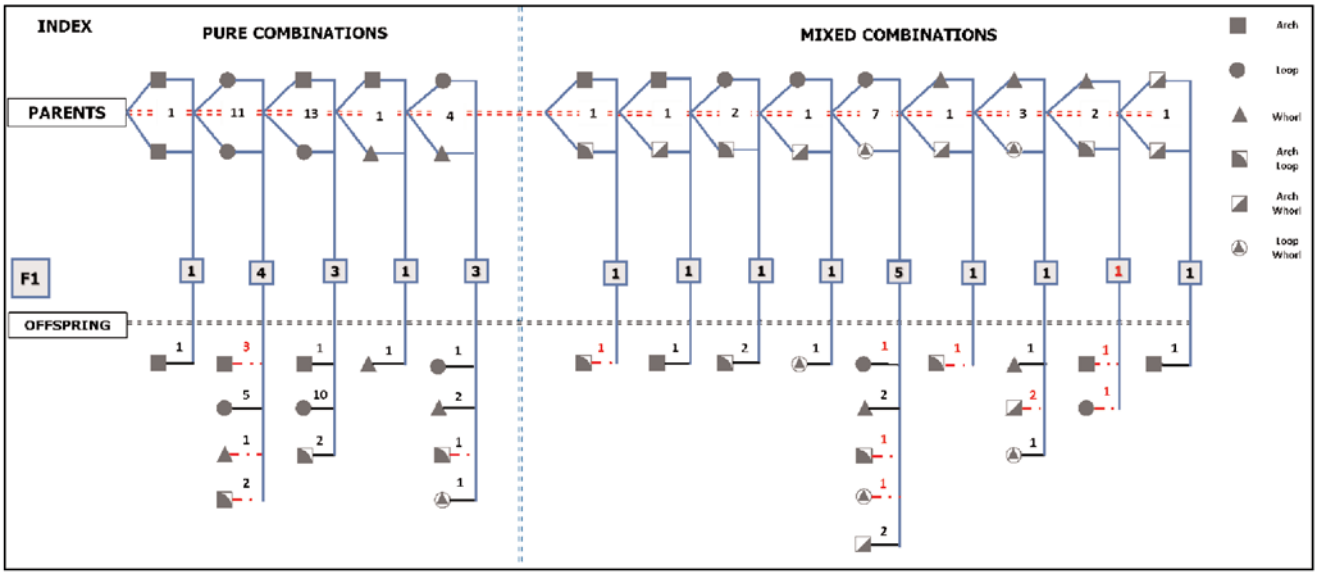

Figure 3. Pedigree tree and offspring patterns from parental combinations on the index finger (offspring conformity to parental combination; black color: yes, red color: no; [38/50=76% possibility of inheritance]). [Color figure can be viewed in the online issue, which is available at www.anatomy.org.tr]

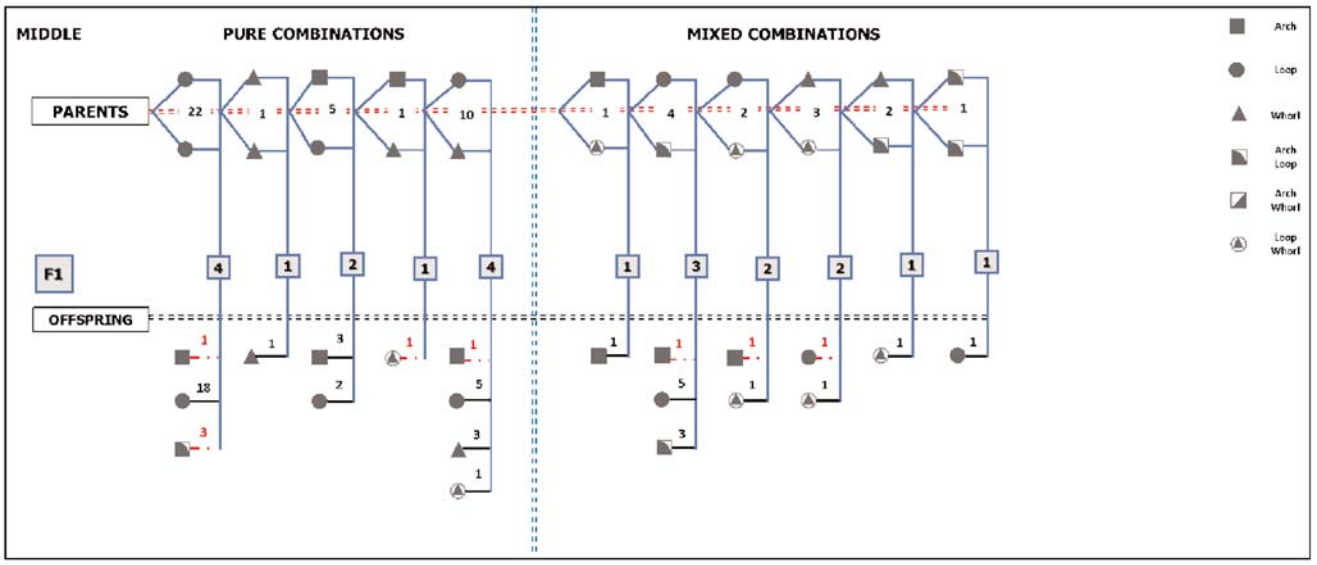

Figure 4. Pedigree tree and offspring patterns from parental combinations on the middle finger (offspring conformity to parental combination; black color: yes, red color: no; [42/50=84% possibility of inheritance]). [Color figure can be viewed in the online issue, which is available at www.anatomy.org.tr]

parental fingerprint combinations on the little finger presented 5 patterns and 92% conformance (46 matching and 4 outliners; **Figure 6**).

Discussion

This study investigated fingerprint combination patterns using a novel classification technique designed for evaluating pattern similarity between parents and their offspring. We observed that loop (L) consistently remained the predominant fingerprint, followed by whorl and then arch; although not generally consistent with whorl (W) and arch (A), because the left index finger had more arch patterns. Eboh,[27] Meril et al.,[28] and Ujaddughe et al.[29] reported similar findings of a higher proportion of loops and arches on left fingers, but whorl on the right.

When the distribution across the family members was compared, there was no difference indicating that

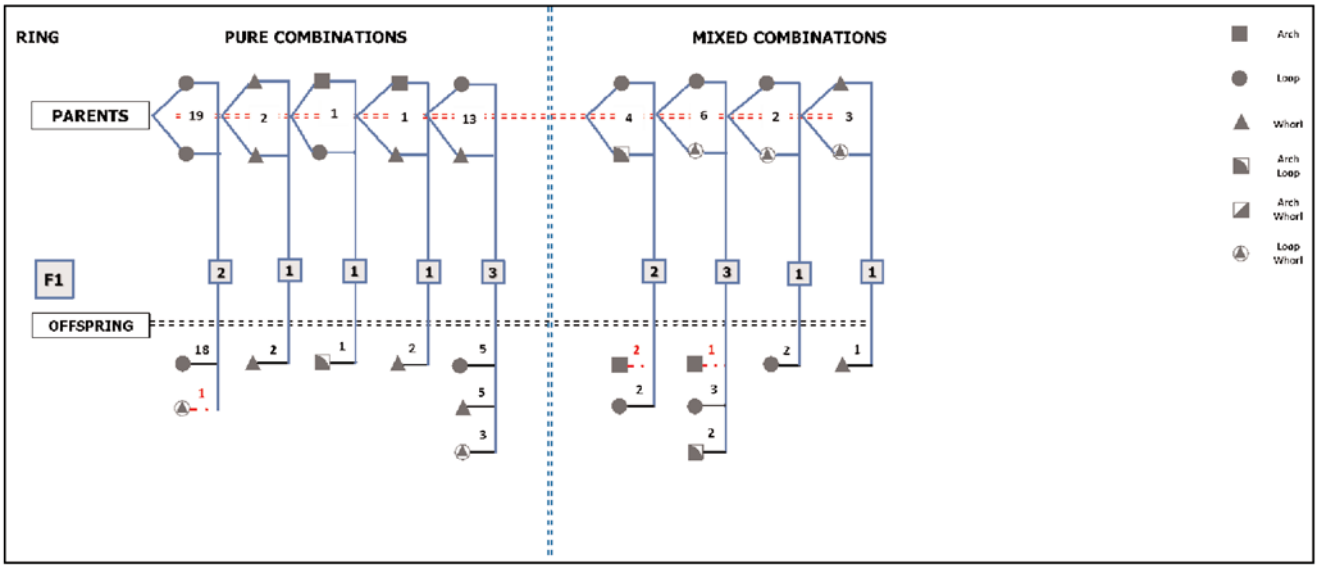

Figure 5. Pedigree tree and offspring patterns from parental combinations on the ring finger (offspring conformity to parental combination; black color: yes, red color: no; [44/50=88% possibility of inheritance]). [Color figure can be viewed in the online issue, which is available at www.anatomy.org.tr]

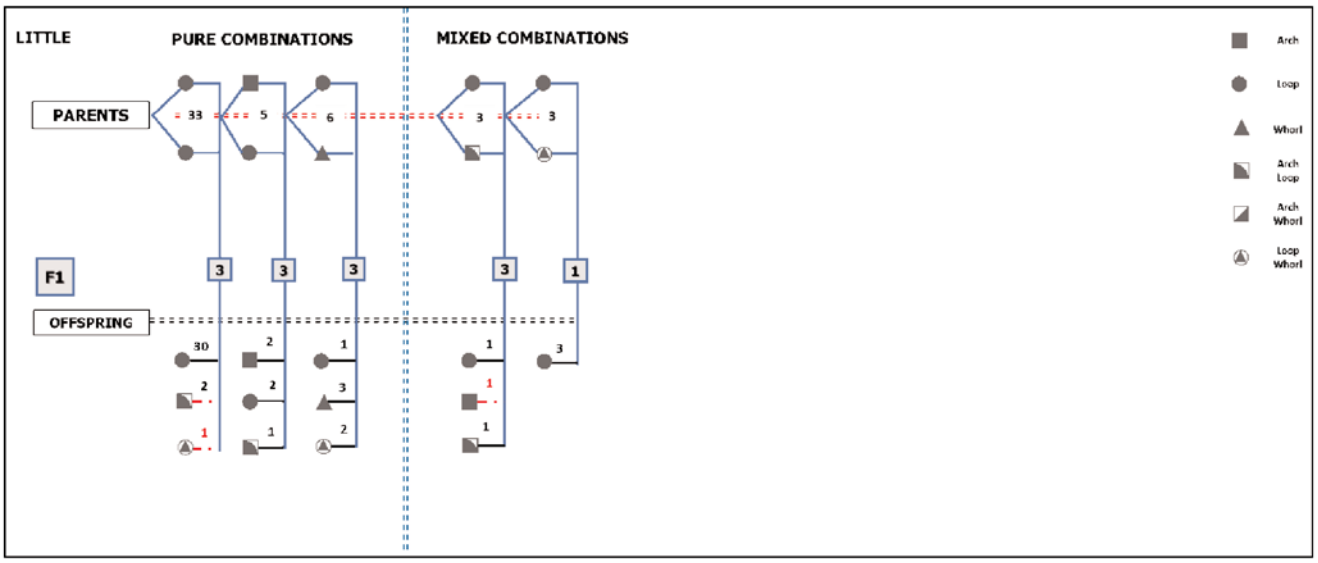

Figure 6. Pedigree tree of offspring patterns from parental combinations on the little finger (offspring conformity to parental combination; black color: yes, red color: no; [46/50=92% possibility of inheritance]). [Color figure can be viewed in the online issue, which is available at www.anatomy.org.tr]

the displayed patterns were generally similar in both parents and the offspring. The total distribution of the pattern on the fingers of parents and offspring was not significant. Thus, the distribution of the fingerprint pattern (types) was a representation of the parental combination.

In evaluating the possibility of inheriting fingerprints, we observed that in the offspring population, the index and ring finger presented all 6 combinations, with an exception to AW, which was absent in all digits of the offspring. However, when present, it was non-conformant to parental combination; thus, suggesting that AW pattern is rarely inherited irrespective of the presentation in the parents. When the parental combination was cross-matched with offspring outcome, the possibility that the offspring presented an accurate pattern from the parental combinations was 78% for the thumb, 76% for the index finger, 84% for the middle finger, 88% for the ring finger, and 92% for the little finger. Observing the various parental combinations in the study population (crossing the fingerprint types of parents in a table for an insight into its possible inheritance pattern), the outcome of some of the fingerprint patterns suggested that the offspring indeed inherited those patterns in an explainable fashion.[30] The findings are suggestive of the possibility of alternated inheritance of these fingerprint patterns, such that parents could display a loop on the right and an arch on the left whereas their offspring will present with arch on the right and loop on the left (alternated inheritance). When both fingers are considered as a single unit, then it is possible that the trait is expressed with a non-side-specific bias like inherited birthmarks, which is often non-location specific.[26]

The findings in this study buttress the fact that fingerprint is a multifactorial trait - that it is genetically determined as well as environmentally influenced.[18–20] Furthermore, as a trait, having three fundamental types (A, L, and W) with several variations, the way offspring will inherit the pattern is not expected to be simple co-dominance as observed in the ABO blood group. This assertion is in line with the report of Hartl and Jones,[31] with the argument that multifactorial traits cannot be studied by means of the simple dominance-recessive pattern because the effects of the segregation of alleles of one gene may be concealed by effects of other genes, and environmental effects may cause identical genotypes to have different phenotypes.

The findings in this study suggest that fingerprint is a tri-allelic non-codominant trait, with a complex phenotypic expression as observed in reduced penetrance. Reduced penetrance exists probably as a result of discrepancies in allelic expression, copy number variation (CNV), or additional genetic variants with modulating influence.[32] Traits that express reduced penetrance follow an autosomal dominant mode of inheritance; although it is also reported to exist in autosomal recessive traits.[33] This is not surprising as studies have suggested that the loop prints have two variants; ulnar and radial forms.[18,25,34] These forms could be a result of mutation of the loop pattern which produced different phenotypic outcomes, which to a large extent depends on

the effect of the allele present.[32] Grundy et al.,[35] Rossetti et al.,[36] Vujic et al.,[37] and Schaaf et al.[38] explained that in certain conditions with an autosomal dominant inheritance, two non-penetrant alleles may express recessivity while copying the normal dominant form of the trait. This study observed that when the parents' pattern had arch (A) and whorl (W) in combination with the loop (L), the offspring almost always expressed L, which happened to be the predominant trait in the studied population. These findings highlight the possibility that the offspring pattern is to a large extent determined by the parental combinations.

Conclusion

The findings of this study reinforce the argument that fingerprints are more genetically determined than environmentally influenced, and that the print patterns are truly passed from parents to offspring. However, the pattern in which it is inherited is rather more complex than the simple Mendelian or co-dominant pattern.

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